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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/776,874A

DATE: 12/12/2001  
TIME: 11:51:23

Input Set : A:\ES.txt  
Output Set: N:\CRF3\12112001\I776874A.raw

ENTERED

3 <110> APPLICANT: Pecker, Iris  
4 Vlodavsky, Israel  
5 Feinstein, Elena  
7 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE  
ACTIVITY AND  
8 EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS  
10 <130> FILE REFERENCE: 01/22603  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/776,874A  
C--> 12 <141> CURRENT FILING DATE: 2001-12-12  
12 <150> PRIOR APPLICATION NUMBER: US 08/922,170  
13 <151> PRIOR FILING DATE: 1997-09-02  
15 <150> PRIOR APPLICATION NUMBER: US 09/109,386  
16 <151> PRIOR FILING DATE: 1998-07-10  
18 <150> PRIOR APPLICATION NUMBER: PCT/US98/17954  
19 <151> PRIOR FILING DATE: 1998-08-31  
21 <160> NUMBER OF SEQ ID NOS: 47  
23 <170> SOFTWARE: PatentIn version 3.1  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 27  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Artificial sequence  
30 <220> FEATURE:  
31 <223> OTHER INFORMATION: synthetic oligonucleotide  
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37 <210> SEQ ID NO: 2  
38 <211> LENGTH: 24  
39 <212> TYPE: DNA  
40 <213> ORGANISM: Artificial sequence  
42 <220> FEATURE:  
43 <223> OTHER INFORMATION: synthetic oligonucleotide  
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49 <210> SEQ ID NO: 3  
50 <211> LENGTH: 23  
51 <212> TYPE: DNA  
52 <213> ORGANISM: Artificial sequence  
54 <220> FEATURE:  
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62 <211> LENGTH: 22  
63 <212> TYPE: DNA  
64 <213> ORGANISM: Artificial sequence  
66 <220> FEATURE:  
67 <223> OTHER INFORMATION: synthetic oligonucleotide  
69 <400> SEQUENCE: 4

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70 gcatcttagc cgtctttctt cg                                22
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75 <212> TYPE: DNA
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78 <220> FEATURE:
79 <223> OTHER INFORMATION: synthetic oligonucleotide
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85 <210> SEQ ID NO: 6
86 <211> LENGTH: 23
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: synthetic oligonucleotide
93 <400> SEQUENCE: 6                                         23
94 ttcgatccca agaaggaatc aac
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 24
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: synthetic oligonucleotide
105 <400> SEQUENCE: 7                                         24
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109 <210> SEQ ID NO: 8
110 <211> LENGTH: 9
111 <212> TYPE: PRT
112 <213> ORGANISM: Homo sapiens
114 <400> SEQUENCE: 8
116 Tyr Gly Pro Asp Val Gly Gln Pro Arg
117 1                    5
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 1721
122 <212> TYPE: DNA
123 <213> ORGANISM: Homo sapiens
125 <400> SEQUENCE: 9
126 ctagagcttt cgactctccg ctgcgcggca gctggcgggg ggagcagcca ggtgagccca    60
128 agatgctgct gcgctcgaag cctgcgctgc cgccgcgcgt gatgctgctg ctctgggggc    120
130 cgctgggtcc cctctccctt ggcgccttgc cccgacctgc gcaagcacag gacgtcgtgg    180
132 acctggactt cttcaccag gagccgctgc acctggtgag cccctcgttc ctgtccgtca    240
134 ccattgacgc caacctggcc acggaccgcg ggttcctcat cctcctgggt tctccaaagc    300
136 ttcgtaacct ggccagaggg ttgtctcctg cgtacctgag gtttggtggc accaagacag    360
138 acttcctaata tttcgatccc aagaaggaat caacctttga agagagaagt tactggcaat    420
140 ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tcctgatgtg gaggagaagt    480
142 tacggttgga atggccctac caggagcaat tgctactccg agaacactac cagaaaaagt    540
144 tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct    600
146 caggactgga cttgatcttt ggcctaaatg cgttattaag aacagcagat ttgcagtgga    660
148 acagttctaa tgctcagttg ctctgggact actgctcttc caaggggtat aacatttctt    720

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150 gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt 780
152 cgcagttagg agaagattat attcaattgc ataaacttct aagaaagtcc accttcaaaa 840
154 atgcaaaaact ctatggtcct gatgttggtc agcctcgaag aaagacggct aagatgctga 900
156 agagcttcct gaaggctggt ggagaagtga ttgattcagt tacatggcat cactactatt 960
158 tgaatggacg gactgctacc agggaagatt ttctaaaccc tgatgtattg gacattttta 1020
160 tttcatctgt gcaaaaagtt ttccaggtgg ttgagagcac caggcctggc aagaaggctc 1080
162 ggtaggaga aacaagctct gcatatggag gcggagcgcc cttgctatcc gacacctttg 1140
164 cagctggctt tatgtggctg gataaattgg gcctgtcagc ccgaatggga atagaagtgg 1200
166 tgatgaggca agtattcttt ggagcaggaa actaccattt agtggatgaa aacttcgatc 1260
168 ctttacctga ttattggcta tctcttctgt tcaagaaatt ggtgggcacc aaggtgttaa 1320
170 tggcaagcgt gcaaggttca aagagaagga agcttcgagt ataccttcat tgcacaaaca 1380
172 ctgacaatcc aaggtataaa gaaggagatt taactctgta tgccataaac ctccataacg 1440
174 tcaccaagta cttgcggtta ccctatcctt tttctaacaa gcaagtggat aaataccttc 1500
176 taagaccttt gggacctcat ggattacttt ccaaactctg ccaactcaat ggtctaactc 1560
178 taaagatggg ggatgatcaa accttgccac ctttaatgga aaaacctctc cggccaggaa 1620
180 gttcactggg cttgccagct ttctcatata gtttttttgt gataagaaat gccaaagttg 1680
182 ctgcttgcat ctgaaaataa aatatactag tcttgacact g 1721

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187 <210> SEQ ID NO: 10

188 <211> LENGTH: 543

189 <212> TYPE: PRT

190 <213> ORGANISM: Homo sapiens

192 <400> SEQUENCE: 10

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194 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
195 1 5 10 15
198 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
199 20 25 30
202 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
203 35 40 45
206 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
207 50 55 60
210 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
211 65 70 75 80
214 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
215 85 90 95
218 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
219 100 105 110
222 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
223 115 120 125
226 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
227 130 135 140
230 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
231 145 150 155 160
234 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
235 165 170 175
238 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
239 180 185 190
242 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
243 195 200 205
246 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn

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247      210      215      220
250 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
251 225      230      235      240
254 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
255      245      250      255
258 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
259      260      265      270
262 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
263      275      280      285
266 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
267      290      295      300
270 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
271 305      310      315      320
274 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
275      325      330      335
278 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
279      340      345      350
282 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
283      355      360      365
286 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
287      370      375      380
290 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
291 385      390      395      400
294 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
295      405      410      415
298 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
299      420      425      430
302 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
303      435      440      445
306 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
307      450      455      460
310 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
311 465      470      475      480
314 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
315      485      490      495
318 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
319      500      505      510
322 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
323      515      520      525
326 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
327      530      535      540

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330 <210> SEQ ID NO: 11  
 331 <211> LENGTH: 1721  
 332 <212> TYPE: DNA  
 333 <213> ORGANISM: Homo sapiens  
 335 <220> FEATURE:  
 336 <221> NAME/KEY: CDS  
 337 <222> LOCATION: (63)..(1691)  
 338 <223> OTHER INFORMATION:

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341 <400> SEQUENCE: 11
342 ctagagcttt cgactctccg ctgctcggca gctggcgggg ggagcagcca ggtgagccca 60
344 ag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ccg ctg atg ctg 107
345 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
346 1 5 10 15
348 ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga 155
349 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
350 20 25 30
352 cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag 203
353 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
354 35 40 45
356 ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc 251
357 Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
358 50 55 60
360 aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag 299
361 Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
362 65 70 75
364 ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt 347
365 Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
366 80 85 90 95
368 ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc 395
369 Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
370 100 105 110
372 ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc 443
373 Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
374 115 120 125
376 aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa 491
377 Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
378 130 135 140
380 tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag 539
381 Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
382 145 150 155
384 ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act 587
385 Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
386 160 165 170 175
388 ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta 635
389 Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
390 180 185 190
392 tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc 683
393 Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
394 195 200 205
396 ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc 731
397 Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
398 210 215 220
400 aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg 779
401 Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
402 225 230 235
404 tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag 827
405 Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\ES.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:3199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47